

SEQUENCE LISTING

<110> C. Frank Bennett
Susan M. Freier

<120> ANTISENSE MODULATION OF SHIP-1 EXPRESSION

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gagccggtca ttccacccag ggggacttca gctgccactg gacacttcaa ttgtacgctg 180

cgaccagttg ccaggaagga gagggctggc aagaaagccg cggcagccgt ggcagggtgt 240

atgggacggt ggacggccag ggccccccc tctctctt tctctctc tctttgttt 300

ggtttctgta atgaggaagt tctccgcagc tcagtttctt ttccctcact gagcgcctga 360

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tgccggccca gccgaggagg cccacgccc cc atg gtc ccc tgc tgg aac cat 533
Met Val Pro Cys Trp Asn His

1 5

ggc aac atc acc cgc tcc aag gcg gag gag ctg ctt tcc agg aca ggc 581
Gly Asn Ile Thr Arg Ser Lys Ala Glu Glu Leu Leu Ser Arg Thr Gly

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aag gac ggg agc ttc ctc gtg cgt gcc agc gag tcc atc tcc cgg gca 629
Lys Asp Gly Ser Phe Leu Val Arg Ala Ser Glu Ser Ile Ser Arg Ala

25 30 35

tac gcg ctc tgc gtg ctg tat cgg aat tgc gtt tac act tac aga att 677
Tyr Ala Leu Cys Val Leu Tyr Arg Asn Cys Val Tyr Thr Tyr Arg Ile

40 45 50 55

ctg ccc aat gaa gat gat aaa ttc act gtt cag gca tcc gaa ggc gtc 725
Leu Pro Asn Glu Asp Asp Lys Phe Thr Val Gln Ala Ser Glu Gly Val

RECEIVED
U.S. PATENT AND TRADEMARK OFFICE
JULY 1998
10:00 AM
1998

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Ser Met Arg Phe Phe Thr Lys Leu Asp Gln Leu Ile Glu Phe Tyr Lys			
75	80	85	
aag gaa aac atg ggg ctg gtg acc cat ctg caa tac cct gtg ccg ctg			821
Lys Glu Asn Met Gly Leu Val Thr His Leu Gln Tyr Pro Val Pro Leu			
90	95	100	
gag gaa gag gac aca ggc gac gac cct gag gag gac aca gaa agt gtc			869
Glu Glu Glu Asp Thr Gly Asp Asp Pro Glu Glu Asp Thr Glu Ser Val			
105	110	115	
gtg tct cca ccc gag ctg ccc cca aga aac atc ccg ctg act gcc agc			917
Val Ser Pro Pro Glu Leu Pro Pro Arg Asn Ile Pro Leu Thr Ala Ser			
120	125	130	135
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Ser Cys Glu Ala Lys Glu Val Pro Phe Ser Asn Glu Asn Pro Arg Ala			
140	145	150	
acc gag acc agc cgg ccg agc ctc tcc gag aca ttg ttc cag cga ctg			1013
Thr Glu Thr Ser Arg Pro Ser Leu Ser Glu Thr Leu Phe Gln Arg Leu			
155	160	165	
caa agc atg gac acc agt ggg ctt cca gaa gag cat ctt aag gcc atc			1061
Gln Ser Met Asp Thr Ser Gly Leu Pro Glu Glu His Leu Lys Ala Ile			
170	175	180	
caa gat tat tta agc act cag ctc gcc cag gac tct gaa ttt gtg aag			1109
Gln Asp Tyr Leu Ser Thr Gln Leu Ala Gln Asp Ser Glu Phe Val Lys			
185	190	195	
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Thr Gly Ser Ser Leu Pro His Leu Lys Lys Leu Thr Thr Leu Leu			
200	205	210	215
tgc aag gag ctc tat gga gaa gtc atc cgg acc ctc cca tcc ctg gag			1205
Cys Lys Glu Leu Tyr Gly Glu Val Ile Arg Thr Leu Pro Ser Leu Glu			
220	225	230	
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Ser Leu Gln Arg Leu Phe Asp Gln Gln Leu Ser Pro Gly Leu Arg Pro			

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Arg Pro Gln Val Pro Gly Glu Ala Asn Pro Ile Asn Met Val Ser Lys			
250	255	260	
ctc agc caa ctg aca agc ctg ttg tca tcc att gaa gac aag gtc aag			1349
Leu Ser Gln Leu Thr Ser Leu Leu Ser Ser Ile Glu Asp Lys Val Lys			
265	270	275	
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Ala Leu Leu His Glu Gly Pro Glu Ser Pro His Arg Pro Ser Leu Ile			
280	285	290	295
cct cca gtc acc ttt gag gtg aag gca gag tct ctg ggg att cct cag			1445
Pro Pro Val Thr Phe Glu Val Lys Ala Glu Ser Leu Gly Ile Pro Gln			
300	305	310	
aaa atg cag ctc aaa gtc gac gtt gag tct ggg aaa ctg atc att aag			1493
Lys Met Gln Leu Lys Val Asp Val Glu Ser Gly Lys Leu Ile Ile Lys			
315	320	325	
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Lys Ser Lys Asp Gly Ser Glu Asp Lys Phe Tyr Ser His Lys Lys Ile			
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ctg cag ctc att aag tca cag aaa ttt ctg aat aag ttg gtg atc ttg			1589
Leu Gln Leu Ile Lys Ser Gln Lys Phe Leu Asn Lys Leu Val Ile Leu			
345	350	355	
gtg gaa aca gag aag gag aag atc ctg cgg aag gaa tat gtt ttt gct			1637
Val Glu Thr Glu Lys Glu Lys Ile Leu Arg Lys Glu Tyr Val Phe Ala			
360	365	370	375
gac tcc aaa aag aga gaa ggc ttc tgc cag ctc ctg cag cag atg aag			1685
Asp Ser Lys Lys Arg Glu Gly Phe Cys Gln Leu Leu Gln Gln Met Lys			
380	385	390	
aac aag cac tca gag cag ccg gag ccc gac atg atc acc atc ttc atc			1733
Asn Lys His Ser Glu Gln Pro Glu Pro Asp Met Ile Thr Ile Phe Ile			
395	400	405	
ggc acc tgg aac atg ggt aac gcc ccc cct ccc aag aag atc acg tcc			1781
Gly Thr Trp Asn Met Gly Asn Ala Pro Pro Lys Lys Ile Thr Ser			

410	415	420	
tgg ttt ctc tcc aag ggg cag gga aag acg cgg gac gac tct gct gac Trp Phe Leu Ser Lys Gly Gln Gly Lys Thr Arg Asp Asp Ser Ala Asp			1829
425	430	435	
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440	445	450	455
agt gag aag gag tgg ctg gag atc ctc aaa cac tcc ctg caa gaa atc Ser Glu Lys Glu Trp Leu Glu Ile Leu Lys His Ser Leu Gln Glu Ile			1925
460	465	470	
acc agt gtg act ttt aaa aca gtc gcc atc cac acg ctc tgg aac atc Thr Ser Val Thr Phe Lys Thr Val Ala Ile His Thr Leu Trp Asn Ile			1973
475	480	485	
cgc atc gtg gtg ctg gcc aag cct gag cac gag aac cgg atc agc cac Arg Ile Val Val Leu Ala Lys Pro Glu His Glu Asn Arg Ile Ser His			2021
490	495	500	
atc tgt act gac aac gtg aag aca ggc att gca aac aca ctg ggg aac Ile Cys Thr Asp Asn Val Lys Thr Gly Ile Ala Asn Thr Leu Gly Asn			2069
505	510	515	
aag gga gcc gtg ggg gtg tcg ttc atg ttc aat gga acc tcc tta ggg Lys Gly Ala Val Gly Val Ser Phe Met Phe Asn Gly Thr Ser Leu Gly			2117
520	525	530	535
ttc gtc aac agc cac ttg act tca gga agt gaa aag aaa ctc agg cga Phe Val Asn Ser His Leu Thr Ser Gly Ser Glu Lys Lys Leu Arg Arg			2165
540	545	550	
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555	560	565	
aag ctg agt ccc ttt aac atc act cac cgc ttc acg cac ctc ttc tgg Lys Leu Ser Pro Phe Asn Ile Thr His Arg Phe Thr His Leu Phe Trp			2261
570	575	580	
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585	590	595	
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600	605	610	2357
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635	640	645	2453
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665	670	675	2549
ccc ctg gtg cac gtg gtg tgt cag tct tat ggc agt acc agc gac atc Pro Leu Val His Val Val Cys Gln Ser Tyr Gly Ser Thr Ser Asp Ile			
680	685	690	2597
695			
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700	705	710	2645
act tcc cag ttt gtc tcc aag aac ggt ccc ggg act gtt gac agc caa Thr Ser Gln Phe Val Ser Lys Asn Gly Pro Gly Thr Val Asp Ser Gln			
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735	740		2741
745			
cag acc aaa ttc tac ctg gag ttc cac tcg agc tgc ttg gag agt ttt Gln Thr Lys Phe Tyr Leu Glu Phe His Ser Ser Cys Leu Glu Ser Phe			
750	755		2789
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			2837

760	765	770	775	
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Val	Val	Lys	Phe	Gly
Glu Thr Leu Pro Lys Leu Lys Pro Ile Ile Ser				
780		785		790
gac cct gag tac ctg cta gac cag cac atc ctc atc agc atc aag tcc				2933
Asp	Pro	Glu	Tyr	Leu
Leu Asp Gln His Ile Leu Ile Ser Ile Lys Ser				
795		800		805
tct gac agc gac gaa tcc tat ggc gag ggc tgc att gcc ctt cgg tta				2981
Ser	Asp	Ser	Asp	Glu
Ser Tyr Gly Glu Gly Cys Ile Ala Leu Arg Leu				
810		815		820
gag gcc aca gaa acg cag ctg ccc atc tac acg cct ctc acc cac cat				3029
Glu	Ala	Thr	Glu	
Thr Gln Leu Pro Ile Tyr Thr Pro Leu Thr His His				
825		830		835
ggg gag ttg aca ggc cac ttc cag ggg gag atc aag ctg cag acc tct				3077
Gly	Glu	Leu	Thr	
Gly His Phe Gln Gly Glu Ile Lys Leu Gln Thr Ser				
840		845		850
cag ggc aag acg agg gag aag ctc tat gac ttt gtg aag acg gag cgt				3125
Gln	Gly	Lys	Thr	
Arg Glu Lys Leu Tyr Asp Phe Val Lys Thr Glu Arg				
860		865		870
gat gaa tcc agt ggg cca aag acc ctg aag agc ctc acc agc cac gac				3173
Asp	Glu	Ser	Ser	
Gly Pro Lys Thr Leu Lys Ser Leu Thr Ser His Asp				
875		880		885
ccc atg aag cag tgg gaa gtc act agc agg gcc cct ccg tgc agt ggc				3221
Pro	Met	Lys	Gln	
Trp Glu Val Thr Ser Arg Ala Pro Pro Cys Ser Gly				
890		895		900
tcc agc atc act gaa atc atc aac ccc aac tac atg gga gtg ggg ccc				3269
Ser	Ser	Ile	Thr	
Glu Ile Ile Asn Pro Asn Tyr Met Gly Val Gly Pro				
905		910		915
ttt ggg cca cca atg ccc ctg cac gtg aag cag acc ttg tcc cct gac				3317
Phe	Gly	Pro	Pro	
Met Pro Leu His Val Lys Gln Thr Leu Ser Pro Asp				
920		925		930
cag cag ccc aca gcc tgg agc tac gac cag ccg ccc aag gac tcc ccg				3365
Gln	Gln	Pro	Thr	
Ala Trp Ser Tyr Asp Gln Pro Pro Lys Asp Ser Pro				

940	945	950	
ctg ggg ccc tgc agg gga gaa agt cct ccg aca cct ccc ggc cag ccg Leu Gly Pro Cys Arg Gly Glu Ser Pro Pro Thr Pro Pro Gly Gln Pro			3413
955	960	965	
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970	975	980	
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985	990	995	
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1100	1105	1110	
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Ile Asn Gln Gln Thr Pro Pro Thr Pro Thr Pro Arg Pro Pro Leu Pro
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Val Lys Ser Pro Ala Val Leu His Leu Gln His Ser Lys Gly Arg Asp
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